

SEQUENCE LISTING

<110> Matuschek, Markus
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Achatz, Brigitte

<120> Method for producing carotenoids or their precursors using
genetically modified organisms of the Blakeslea genus,
carotenoids or their precursors produced by said method and use
thereof

<130> 13311-00009-US

<150> PCT/EP2004/000099
<151> 2004-01-09

<150> DE 103 00 649.4
<151> 2003-01-09

<150> DE 103 41 271.9
<151> 2003-09-08

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120

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Met Gln Leu Ala
1

177

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Ala Thr Val Met Leu Glu Gln Leu Thr Gly Ser Ala Glu Ala Leu Lys
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225

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Glu Lys Glu Lys Glu Val Ala Gly Ser Ser Asp Val Leu Arg Thr Trp
25 30 35

273

gcg acc cag tac tcg ctt ccg tca gaa gag tca gac gcg gcc cgc ccg
Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp Ala Ala Arg Pro
40 45 50

321

gga ctg aag aat gcc tac aag cca cca cct tcc gac aca aag ggc atc
Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp Thr Lys Gly Ile
55 60 65

369

aca atg gcg cta cgt gtc atc ggc tcc tgg gcc gca gtg ttc ctc cac
Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala Val Phe Leu His
70 75 80

417

gcc att ttt caa atc aag ctt ccg acc tcc ttg gac cag ctg cac tgg	465
Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp Gln Leu His Trp	
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ctg ccc gtg tca gat gcc aca gct cag ctg gtt agc ggc acg agc agc	513
Leu Pro Val Ser Asp Ala Thr Ala Gln Leu Val Ser Gly Thr Ser Ser	
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Leu Leu Asp Ile Val Val Val Phe Phe Val Leu Glu Phe Leu Tyr Thr	
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Gly Leu Phe Ile Thr Thr His Asp Ala Met His Gly Thr Ile Ala Met	
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Arg Asn Arg Gln Leu Asn Asp Phe Leu Gly Arg Val Cys Ile Ser Leu	
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Tyr Ala Trp Phe Asp Tyr Asn Met Leu His Arg Lys His Trp Glu His	
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His Asn His Thr Gly Glu Val Gly Lys Asp Pro Asp Phe His Arg Gly	
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Asn Pro Gly Ile Val Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met	
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Ser Met Trp Gln Phe Ala Arg Leu Ala Trp Trp Thr Val Val Met Gln	
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ccc atc ctg tcc gcc ttc cgc ttg ttc tac ttt ggc acg tac atg ccc	945
Pro Ile Leu Ser Ala Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Met Pro	
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cac aag cct gag cct ggc gcc gcg tca ggc tct tca cca gcc gtc atg	993
His Lys Pro Glu Pro Gly Ala Ala Ser Gly Ser Ser Pro Ala Val Met	
265 270 275	
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Asn Trp Trp Lys Ser Arg Thr Ser Gln Ala Ser Asp Leu Val Ser Phe	
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Leu Thr Cys Tyr His Phe Asp Leu His Trp Glu His His Arg Trp Pro	
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 Phe Ala Pro Trp Trp Glu Leu Pro Asn Cys Arg Arg Leu Ser Gly Arg
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 Gly Leu Val Pro Ala
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<212> PRT

<213> Haematococcus pluvialis

<400> 12

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Leu Arg Thr Trp Ala Thr Gln Tyr Ser Leu Pro Ser Glu Glu Ser Asp
 35 40 45

Ala Ala Arg Pro Gly Leu Lys Asn Ala Tyr Lys Pro Pro Pro Ser Asp
 50 55 60

Thr Lys Gly Ile Thr Met Ala Leu Arg Val Ile Gly Ser Trp Ala Ala
 65 70 75 80

Val Phe Leu His Ala Ile Phe Gln Ile Lys Leu Pro Thr Ser Leu Asp

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315

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<211> 1662

<212> DNA

<213> Haematococcus pluvialis

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<222> (168)..(1130)

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ctccgtcctc tgccaaatct cgcgtcgggg cctgcctaag tcgaaga atg cac gtc 176
Met His Val
1

gca tcg gca cta atg gtc gag cag aaa ggc agt gag gca gct gct tcc 224
Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala Ala Ala Ser
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agc cca gac gtc ttg aga gcg tgg gcg aca cag tat cac atg cca tcc 272
Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His Met Pro Ser
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gag tcg tca gac gca gct cgt cct gcg cta aag cac gcc tac aaa cct 320
Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala Tyr Lys Pro
40 45 50

cca gca tct gac gcc aag ggc atc acg atg gcg ctg acc atc att ggc 368
Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr Ile Ile Gly
55 60 65

acc tgg acc gca gtg ttt tta cac gca ata ttt caa atc agg cta ccg 416
Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile Arg Leu Pro
70 75 80

aca tcc atg gac cag ctt cac tgg ttg cct gtg tcc gaa gcc aca gcc 464
Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu Ala Thr Ala
85 90 95

cag ctt ttg ggc gga agc agc agc cta ctg cac atc gct gca gtc ttc 512
Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala Ala Val Phe
100 105 110 115

att gta ctt gag ttc ctg tac act ggt cta ttc atc acc aca cat gac 560
Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr Thr His Asp
120 125 130

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tct gat gtg atg agt ttc ctg aca tgc tac cac ttt gac ctg cac tgg Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp Leu His Trp 280 285 290	1040
gag cac cac agg tgg ccc ttt gcc ccc tgg tgg cag ctg ccc cac tgc Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu Pro His Cys 295 300 305	1088
cgc cgc ctg tcc ggg cgt ggc ctg gtg cct gcc ttg gca tga Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala 310 315 320	1130
cctgggtccct ccgctggtga cccagcgtct gcacaagagt gtcattgctac aggggtgctgc	1190
ggccagtggc agcgcagtgc actctcagcc tgtatggggc taccgctgtg ccactgagca	1250
ctgggcatgc cactgagcac tgggcgtgct actgagcaat gggcgtgcta ctgagcaatg	1310
ggcgtgctac tgacaatggg cgtgctactg gggctctggca gtggctagga tggagtttga	1370

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tgcattcagt agcgggtggcc aacgtcatgt ggatgggtgga agtgctgagg ggtttaggca 1430
gccgggcattt gagaggggcta agttataaat cgcattgctgc tcatgcgcac atatctgcac 1490
acagccagggg aaatcccttc gagagtgatt atgggacact tgtattgggt tcgtgctatt 1550
gttttattca gcagcagtac ttagtgaggg tgagagcagg gtggtgagag tggagtgagt 1610
gagtatgaac ctggtcagcg aggtgaacag cctgtaatga atgactctgt ct 1662

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<210> 14
<211> 320
<212> PRT
<213> Haematococcus pluvialis

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<400> 14

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Met His Val Ala Ser Ala Leu Met Val Glu Gln Lys Gly Ser Glu Ala
1          5          10          15

```

```

Ala Ala Ser Ser Pro Asp Val Leu Arg Ala Trp Ala Thr Gln Tyr His
          20          25          30

```

```

Met Pro Ser Glu Ser Ser Asp Ala Ala Arg Pro Ala Leu Lys His Ala
          35          40          45

```

```

Tyr Lys Pro Pro Ala Ser Asp Ala Lys Gly Ile Thr Met Ala Leu Thr
          50          55          60

```

```

Ile Ile Gly Thr Trp Thr Ala Val Phe Leu His Ala Ile Phe Gln Ile
65          70          75          80

```

```

Arg Leu Pro Thr Ser Met Asp Gln Leu His Trp Leu Pro Val Ser Glu
          85          90          95

```

```

Ala Thr Ala Gln Leu Leu Gly Gly Ser Ser Ser Leu Leu His Ile Ala
          100          105          110

```

```

Ala Val Phe Ile Val Leu Glu Phe Leu Tyr Thr Gly Leu Phe Ile Thr
          115          120          125

```

```

Thr His Asp Ala Met His Gly Thr Ile Ala Leu Arg His Arg Gln Leu
          130          135          140

```

```

Asn Asp Leu Leu Gly Asn Ile Cys Ile Ser Leu Tyr Ala Trp Phe Asp
145          150          155          160

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Tyr Ser Met Leu His Arg Lys His Trp Glu His His Asn His Thr Gly
 165 170 175

Glu Val Gly Lys Asp Pro Asp Phe His Lys Gly Asn Pro Gly Leu Val
 180 185 190

Pro Trp Phe Ala Ser Phe Met Ser Ser Tyr Met Ser Leu Trp Gln Phe
 195 200 205

Ala Arg Leu Ala Trp Trp Ala Val Val Met Gln Met Leu Gly Ala Pro
 210 215 220

Met Ala Asn Leu Leu Val Phe Met Ala Ala Ala Pro Ile Leu Ser Ala
 225 230 235 240

Phe Arg Leu Phe Tyr Phe Gly Thr Tyr Leu Pro His Lys Pro Glu Pro
 245 250 255

Gly Pro Ala Ala Gly Ser Gln Val Met Ala Trp Phe Arg Ala Lys Thr
 260 265 270

Ser Glu Ala Ser Asp Val Met Ser Phe Leu Thr Cys Tyr His Phe Asp
 275 280 285

Leu His Trp Glu His His Arg Trp Pro Phe Ala Pro Trp Trp Gln Leu
 290 295 300

Pro His Cys Arg Arg Leu Ser Gly Arg Gly Leu Val Pro Ala Leu Ala
 305 310 315 320

<210> 15
 <211> 729
 <212> DNA
 <213> Agrobacterium aurantiacum

<220>
 <221> CDS
 <222> (1) .. (729)

<400> 15
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 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
 1 5 10 15

atc gtc tcg ggc ggc atc atc gcc gct tgg ctg gcc ctg cat gtg cat Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His 20 25 30	96
gcg ctg tgg ttt ctg gac gca gcg gcg cat ccc atc ctg gcg atc gca Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala 35 40 45	144
aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala 50 55 60	192
cat gac gcg atg cac ggg tcg gtg gtg ccg ggg cgt ccg cgc gcc aat His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn 65 70 75 80	240
gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp 85 90 95	288
cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr 100 105 110	336
gac gac gac ccc gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala 115 120 125	384
cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro 130 135 140	432
gtc atc gtg acg gtc tat gcg ctg atc ctt ggg gat cgc tgg atg tac Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr 145 150 155 160	480
gtg gtc ttc tgg ccg ctg ccg tcg atc ctg gcg tcg atc cag ctg ttc Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe 165 170 175	528
gtg ttc ggc acc tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro 180 185 190	576
gac cgc cac aat gcg cgg tcg tcg cgg atc agc gac ccc gtg tcg ctg Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu 195 200 205	624
ctg acc tgc ttt cac ttt ggc ggt tat cat cac gaa cac cac ctg cac Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His 210 215 220	672
ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp 225 230 235 240	720
acc gca tga	729

Thr Ala

<210> 16
 <211> 242
 <212> PRT
 <213> Agrobacterium aurantiacum
 <400> 16

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
 1 5 10 15

Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Ile Ala
 35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
 115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro

180	185	190
Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu		
195	200	205
Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His		
210	215	220
Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp		
225	230	235 240

Thr Ala

<210> 17
 <211> 1631
 <212> DNA
 <213> *Alcaligenes* sp.

<220>
 <221> CDS
 <222> (99)..(827)

<400> 17
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 ccggtctagg ctgtcgccct acgcagcagg agtttcgg atg tcc gga cgg aag cct 116
 Met Ser Gly Arg Lys Pro
 1 5
 ggc aca act ggc gac acg atc gtc aat ctc ggt ctg acc gcc gcg atc 164
 Gly Thr Thr Gly Asp Thr Ile Val Asn Leu Gly Leu Thr Ala Ala Ile
 10 15 20
 ctg ctg tgc tgg ctg gtc ctg cac gcc ttt acg cta tgg ttg cta gat 212
 Leu Leu Cys Trp Leu Val Leu His Ala Phe Thr Leu Trp Leu Leu Asp
 25 30 35
 gcg gcc gcg cat ccg ctg ctt gcc gtg ctg tgc ctg gct ggg ctg acc 260
 Ala Ala Ala His Pro Leu Leu Ala Val Leu Cys Leu Ala Gly Leu Thr
 40 45 50
 tgg ctg tgc gtc ggg ctg ttc atc atc gcg cat gac gca atg cac ggg 308
 Trp Leu Ser Val Gly Leu Phe Ile Ile Ala His Asp Ala Met His Gly
 55 60 65 70
 tcc gtg gtg ccg ggg cgg ccg cgc gcc aat gcg gcg atc ggg caa ctg 356
 Ser Val Val Pro Gly Arg Pro Arg Ala Asn Ala Ala Ile Gly Gln Leu
 75 80 85
 gcg ctg tgg ctc tat gcg ggg ttc tgc tgg ccc aag ctg atc gcc aag 404

Ala	Leu	Trp	Leu	Tyr	Ala	Gly	Phe	Ser	Trp	Pro	Lys	Leu	Ile	Ala	Lys		
			90					95					100				
cac	atg	acg	cat	cac	cgg	cac	gcc	ggc	acc	gac	aac	gat	ccc	gat	ttc	452	
His	Met	Thr	His	His	Arg	His	Ala	Gly	Thr	Asp	Asn	Asp	Pro	Asp	Phe		
		105					110					115					
ggc	cac	gga	ggg	ccc	gtg	cgc	tgg	tac	ggc	agc	ttc	gtc	tcc	acc	tat	500	
Gly	His	Gly	Gly	Pro	Val	Arg	Trp	Tyr	Gly	Ser	Phe	Val	Ser	Thr	Tyr		
		120				125					130						
ttc	ggc	tgg	cga	gag	gga	ctg	ctg	cta	ccg	gtg	atc	gtc	acc	acc	tat	548	
Phe	Gly	Trp	Arg	Glu	Gly	Leu	Leu	Leu	Pro	Val	Ile	Val	Thr	Thr	Tyr		
135					140					145					150		
gcg	ctg	atc	ctg	ggc	gat	cgc	tgg	atg	tat	gtc	atc	ttc	tgg	ccg	gtc	596	
Ala	Leu	Ile	Leu	Gly	Asp	Arg	Trp	Met	Tyr	Val	Ile	Phe	Trp	Pro	Val		
				155				160						165			
ccg	gcc	gtt	ctg	gcg	tcg	atc	cag	att	ttc	gtc	ttc	gga	act	tgg	ctg	644	
Pro	Ala	Val	Leu	Ala	Ser	Ile	Gln	Ile	Phe	Val	Phe	Gly	Thr	Trp	Leu		
			170					175					180				
ccc	cac	cgc	ccg	gga	cat	gac	gat	ttt	ccc	gac	cgg	cac	aac	gcg	agg	692	
Pro	His	Arg	Pro	Gly	His	Asp	Asp	Phe	Pro	Asp	Arg	His	Asn	Ala	Arg		
		185					190					195					
tcg	acc	ggc	atc	ggc	gac	ccg	ttg	tca	cta	ctg	acc	tgc	ttc	cat	ttc	740	
Ser	Thr	Gly	Ile	Gly	Asp	Pro	Leu	Ser	Leu	Leu	Thr	Cys	Phe	His	Phe		
		200				205					210						
ggc	ggc	tat	cac	cac	gaa	cat	cac	ctg	cat	ccg	cat	gtg	ccg	tgg	tgg	788	
Gly	Gly	Tyr	His	His	Glu	His	His	Leu	His	Pro	His	Val	Pro	Trp	Trp		
215					220					225					230		
cgc	ctg	cct	cgt	aca	cgc	aag	acc	gga	ggc	cgc	gca	tga	cgcaattcct			837	
Arg	Leu	Pro	Arg	Thr	Arg	Lys	Thr	Gly	Gly	Arg	Ala						
				235				240									
cattg	tcgtg		gcgacag	tc	tcgtgat	gga		gctgacc	gcc		tattccg	tc	accgctg	gat		897	
tatgcac	ggc		cccctag	gct	ggggctg	gca		caagtcc	cat		cacgaag	agc	acgaccac	gc		957	
gttgga	gagaag		aacgac	ctct	acggcgt	cg		cttcgc	ggtg		ctggcgac	ga	tcctcttc	ac		1017	
cg	tg	ggcgcc		tattggt	ggc	cggtg	ctgtg	gtggat	cgcc		ctgggc	atga	cggtctat	gg		1077	
gttgat	ctat		ttcat	ctc	gc	acgac	ggg	gct	gcat	caa	cgctg	ggcc	gt	ttc	ggtatat	1137	
tc	gc	ggcg		ggctatt	ttcc	gcag	gct	cta	ccaag	ctcat	cg	ctgc	acc	acgc	ggtcga	1197	
ggggc	ggggac		cactgc	gtca	gcttc	ggctt		catctat	gcc		ccacc	cg	tgg	acaag	ctgaa	1257	
gcaggat	ctg		aagc	gg	tc	gg		gtgt	c	ctgc		cccc	caggac	gagc	gtcc	gt	1317
gatccc	ggcg		tg	gcgc	atg	aaat	ccga	cg	tgct	gctggc		agggg	ccggc	cttg	ccaacg	1377	

gactgatcgc gctggcgatc cgcaaggcgc ggcccgcacct tcgcgtgctg ctgctggacc 1437
 gtgcggcggg cgcctcggac gggcatactt ggtcctgccca cgacaccgat ttggcgccgc 1497
 actggctgga ccgcctgaag ccgatcaggc gtggcgactg gcccgatcag gaggtgcggt 1557
 tcccagacca ttgcggaagg ctccggggccg gatatggctc gatcgacggg cgggggctga 1617
 tgcgtgcggt gacc 1631

<210> 18
 <211> 242
 <212> PRT
 <213> *Alcaligenes* sp.

<400> 18

Met Ser Gly Arg Lys Pro Gly Thr Thr Gly Asp Thr Ile Val Asn Leu
 1 5 10 15

Gly Leu Thr Ala Ala Ile Leu Leu Cys Trp Leu Val Leu His Ala Phe
 20 25 30

Thr Leu Trp Leu Leu Asp Ala Ala Ala His Pro Leu Leu Ala Val Leu
 35 40 45

Cys Leu Ala Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala Ile Gly Gln Leu Ala Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

Pro Lys Leu Ile Ala Lys His Met Thr His His Arg His Ala Gly Thr
 100 105 110

Asp Asn Asp Pro Asp Phe Gly His Gly Gly Pro Val Arg Trp Tyr Gly
 115 120 125

Ser Phe Val Ser Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

Val Ile Val Thr Thr Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

Val Ile Phe Trp Pro Val Pro Ala Val Leu Ala Ser Ile Gln Ile Phe
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Asp Phe Pro
 180 185 190

Asp Arg His Asn Ala Arg Ser Thr Gly Ile Gly Asp Pro Leu Ser Leu
 195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

Pro His Val Pro Trp Trp Arg Leu Pro Arg Thr Arg Lys Thr Gly Gly
 225 230 235 240

Arg Ala

<210> 19
 <211> 729
 <212> DNA
 <213> *Paracoccus marcusii*

<220>
 <221> CDS
 <222> (1)..(729)

<400> 19
 atg agc gca cat gcc ctg ccc aag gca gat ctg acc gcc aca agc ctg 48
 Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
 1 5 10 15
 atc gtc tcg ggc ggc atc atc gcc gca tgg ctg gcc ctg cat gtg cat 96
 Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His
 20 25 30
 gcg ctg tgg ttt ctg gac gcg gcg gcc cat ccc atc ctg gcg gtc gcg 144
 Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala
 35 40 45
 aat ttc ctg ggg ctg acc tgg ctg tcg gtc gga ttg ttc atc atc gcg 192
 Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60
 cat gac gcg atg cac ggg tcg gtc gtg ccg ggg cgt ccg cgc gcc aat 240
 His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

gcg gcg atg ggc cag ctt gtc ctg tgg ctg tat gcc gga ttt tcg tgg	288
Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp	
85 90 95	
cgc aag atg atc gtc aag cac atg gcc cat cac cgc cat gcc gga acc	336
Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr	
100 105 110	
gac gac gac cca gat ttc gac cat ggc ggc ccg gtc cgc tgg tac gcc	384
Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala	
115 120 125	
cgc ttc atc ggc acc tat ttc ggc tgg cgc gag ggg ctg ctg ctg ccc	432
Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro	
130 135 140	
gtc atc gtg acg gtc tat gcg ctg atc ctg ggg gat cgc tgg atg tac	480
Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr	
145 150 155 160	
gtg gtc ttc tgg ccg ttg ccg tcg atc ctg gcg tcg atc cag ctg ttc	528
Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe	
165 170 175	
gtg ttc ggc act tgg ctg ccg cac cgc ccc ggc cac gac gcg ttc ccg	576
Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro	
180 185 190	
gac cgc cat aat gcg cgg tcg tcg cgg atc agc gac cct gtg tcg ctg	624
Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu	
195 200 205	
ctg acc tgc ttt cat ttt ggc ggt tat cat cac gaa cac cac ctg cac	672
Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His	
210 215 220	
ccg acg gtg ccg tgg tgg cgc ctg ccc agc acc cgc acc aag ggg gac	720
Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp	
225 230 235 240	
acc gca tga	729
Thr Ala	

<210> 20
 <211> 242
 <212> PRT
 <213> *Paracoccus marcusii*

<400> 20

Met Ser Ala His Ala Leu Pro Lys Ala Asp Leu Thr Ala Thr Ser Leu
1 5 10 15

Ile Val Ser Gly Gly Ile Ile Ala Ala Trp Leu Ala Leu His Val His

20

25

30

Ala Leu Trp Phe Leu Asp Ala Ala Ala His Pro Ile Leu Ala Val Ala
 35 40 45

Asn Phe Leu Gly Leu Thr Trp Leu Ser Val Gly Leu Phe Ile Ile Ala
 50 55 60

His Asp Ala Met His Gly Ser Val Val Pro Gly Arg Pro Arg Ala Asn
 65 70 75 80

Ala Ala Met Gly Gln Leu Val Leu Trp Leu Tyr Ala Gly Phe Ser Trp
 85 90 95

Arg Lys Met Ile Val Lys His Met Ala His His Arg His Ala Gly Thr
 100 105 110

Asp Asp Asp Pro Asp Phe Asp His Gly Gly Pro Val Arg Trp Tyr Ala
 115 120 125

Arg Phe Ile Gly Thr Tyr Phe Gly Trp Arg Glu Gly Leu Leu Leu Pro
 130 135 140

Val Ile Val Thr Val Tyr Ala Leu Ile Leu Gly Asp Arg Trp Met Tyr
 145 150 155 160

Val Val Phe Trp Pro Leu Pro Ser Ile Leu Ala Ser Ile Gln Leu Phe
 165 170 175

Val Phe Gly Thr Trp Leu Pro His Arg Pro Gly His Asp Ala Phe Pro
 180 185 190

Asp Arg His Asn Ala Arg Ser Ser Arg Ile Ser Asp Pro Val Ser Leu
 195 200 205

Leu Thr Cys Phe His Phe Gly Gly Tyr His His Glu His His Leu His
 210 215 220

Pro Thr Val Pro Trp Trp Arg Leu Pro Ser Thr Arg Thr Lys Gly Asp
 225 230 235 240

Thr Ala

<210> 21
 <211> 1629
 <212> DNA
 <213> *Synechocystis* sp.

<220>
 <221> CDS
 <222> (1)..(1629)

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<400> 21
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Met Ile Thr Thr Asp Val Val Ile Ile Gly Ala Gly His Asn Gly Leu
1           5           10           15

gtc tgt gca gcc tat ttg ctc caa cgg ggc ttg ggg gtg acg tta cta      96
Val Cys Ala Ala Tyr Leu Leu Gln Arg Gly Leu Gly Val Thr Leu Leu
           20           25           30

gaa aag cgg gaa gta cca ggg ggg gcg gcc acc aca gaa gct ctc atg      144
Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met
           35           40           45

ccg gag cta tcc ccc cag ttt cgc ttt aac cgc tgt gcc att gac cac      192
Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His
           50           55           60

gaa ttt atc ttt ctg ggg ccg gtg ttg cag gag cta aat tta gcc cag      240
Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln
65           70           75           80

tat ggt ttg gaa tat tta ttt tgt gac ccc agt gtt ttt tgt ccg ggg      288
Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly
           85           90           95

ctg gat ggc caa gct ttt atg agc tac cgt tcc cta gaa aaa acc tgt      336
Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys
           100           105           110

gcc cac att gcc acc tat agc ccc cga gat gcg gaa aaa tat cgg caa      384
Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln
           115           120           125

ttt gtc aat tat tgg acg gat ttg ctc aac gct gtc cag cct gct ttt      432
Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe
           130           135           140

aat gct ccg ccc cag gct tta cta gat tta gcc ctg aac tat ggt tgg      480
Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp
145           150           155           160

gaa aac tta aaa tcc gtg ctg gcg atc gcc ggg tcg aaa acc aag gcg      528
Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala

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165	170	175	
ttg gat ttt atc cgc act atg atc ggc tcc ccg gaa gat gtg ctc aat Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn 180 185 190			576
gaa tgg ttc gac agc gaa cgg gtt aaa gct cct tta gct aga cta tgt Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys 195 200 205			624
tcg gaa att ggc gct ccc cca tcc caa aag ggt agt agc tcc ggc atg Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met 210 215 220			672
atg atg gtg gcc atg cgg cat ttg gag gga att gcc aga cca aaa gga Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly 225 230 235 240			720
ggc act gga gcc ctc aca gaa gcc ttg gtg aag tta gtg caa gcc caa Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln 245 250 255			768
ggg gga aaa atc ctc act gac caa acc gtc aaa cgg gta ttg gtg gaa Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu 260 265 270			816
aac aac cag gcg atc ggg gtg gag gta gct aac gga gaa cag tac cgg Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg 275 280 285			864
gcc aaa aaa ggc gtg att tct aac atc gat gcc cgc cgt tta ttt ttg Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu 290 295 300			912
caa ttg gtg gaa ccg ggg gcc cta gcc aag gtg aat caa aac cta ggg Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly 305 310 315 320			960
gaa cga ctg gaa cgg cgc act gtg aac aat aac gaa gcc att tta aaa Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys 325 330 335			1008
atc gat tgt gcc ctc tcc ggt tta ccc cac ttc act gcc atg gcc ggg Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly 340 345 350			1056
ccg gag gat cta acg gga act att ttg att gcc gac tcg gta cgc cat Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His 355 360 365			1104
gtc gag gaa gcc cac gcc ctc att gcc ttg ggg caa att ccc gat gct Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala 370 375 380			1152
aat ccg tct tta tat ttg gat att ccc act gta ttg gac ccc acc atg			1200

Asn	Pro	Ser	Leu	Tyr	Leu	Asp	Ile	Pro	Thr	Val	Leu	Asp	Pro	Thr	Met	
385					390					395					400	
gcc	ccc	cct	ggg	cag	cac	acc	ctc	tgg	atc	gaa	ttt	ttt	gcc	ccc	tac	1248
Ala	Pro	Pro	Gly	Gln	His	Thr	Leu	Trp	Ile	Glu	Phe	Phe	Ala	Pro	Tyr	
			405					410					415			
cgc	atc	gcc	ggg	ttg	gaa	ggg	aca	ggg	tta	atg	ggc	aca	ggg	tgg	acc	1296
Arg	Ile	Ala	Gly	Leu	Glu	Gly	Thr	Gly	Leu	Met	Gly	Thr	Gly	Trp	Thr	
			420					425					430			
gat	gag	tta	aag	gaa	aaa	gtg	gcg	gat	cgg	gtg	att	gat	aaa	tta	acg	1344
Asp	Glu	Leu	Lys	Glu	Lys	Val	Ala	Asp	Arg	Val	Ile	Asp	Lys	Leu	Thr	
		435					440					445				
gac	tat	gcc	cct	aac	cta	aaa	tct	ctg	atc	att	ggg	cgc	cga	gtg	gaa	1392
Asp	Tyr	Ala	Pro	Asn	Leu	Lys	Ser	Leu	Ile	Ile	Gly	Arg	Arg	Val	Glu	
	450					455					460					
agt	ccc	gcc	gaa	ctg	gcc	caa	cgg	ctg	gga	agt	tac	aac	ggc	aat	gtc	1440
Ser	Pro	Ala	Glu	Leu	Ala	Gln	Arg	Leu	Gly	Ser	Tyr	Asn	Gly	Asn	Val	
465					470				475						480	
tat	cat	ctg	gat	atg	agt	ttg	gac	caa	atg	atg	ttc	ctc	cgg	cct	cta	1488
Tyr	His	Leu	Asp	Met	Ser	Leu	Asp	Gln	Met	Met	Phe	Leu	Arg	Pro	Leu	
			485					490					495			
ccg	gaa	att	gcc	aac	tac	caa	acc	ccc	atc	aaa	aat	ctt	tac	tta	aca	1536
Pro	Glu	Ile	Ala	Asn	Tyr	Gln	Thr	Pro	Ile	Lys	Asn	Leu	Tyr	Leu	Thr	
			500					505					510			
ggg	gcg	ggg	acc	cat	ccc	ggg	ggc	tcc	ata	tca	ggg	atg	ccc	ggg	aga	1584
Gly	Ala	Gly	Thr	His	Pro	Gly	Gly	Ser	Ile	Ser	Gly	Met	Pro	Gly	Arg	
		515					520					525				
aat	tgc	gct	cgg	gtc	ttt	tta	aaa	caa	caa	cgt	cgt	ttt	tgg	taa		1629
Asn	Cys	Ala	Arg	Val	Phe	Leu	Lys	Gln	Gln	Arg	Arg	Phe	Trp			
	530					535					540					

<210> 22
 <211> 542
 <212> PRT
 <213> Synechocystis sp.

<400> 22

Met	Ile	Thr	Thr	Asp	Val	Val	Ile	Ile	Gly	Ala	Gly	His	Asn	Gly	Leu
1				5					10					15	

Val	Cys	Ala	Ala	Tyr	Leu	Leu	Gln	Arg	Gly	Leu	Gly	Val	Thr	Leu	Leu
		20						25					30		

Glu Lys Arg Glu Val Pro Gly Gly Ala Ala Thr Thr Glu Ala Leu Met

35	40	45
Pro Glu Leu Ser Pro Gln Phe Arg Phe Asn Arg Cys Ala Ile Asp His		
50	55	60
Glu Phe Ile Phe Leu Gly Pro Val Leu Gln Glu Leu Asn Leu Ala Gln		
65	70	75 80
Tyr Gly Leu Glu Tyr Leu Phe Cys Asp Pro Ser Val Phe Cys Pro Gly		
	85	90 95
Leu Asp Gly Gln Ala Phe Met Ser Tyr Arg Ser Leu Glu Lys Thr Cys		
	100	105 110
Ala His Ile Ala Thr Tyr Ser Pro Arg Asp Ala Glu Lys Tyr Arg Gln		
	115	120 125
Phe Val Asn Tyr Trp Thr Asp Leu Leu Asn Ala Val Gln Pro Ala Phe		
	130	135 140
Asn Ala Pro Pro Gln Ala Leu Leu Asp Leu Ala Leu Asn Tyr Gly Trp		
145	150	155 160
Glu Asn Leu Lys Ser Val Leu Ala Ile Ala Gly Ser Lys Thr Lys Ala		
	165	170 175
Leu Asp Phe Ile Arg Thr Met Ile Gly Ser Pro Glu Asp Val Leu Asn		
	180	185 190
Glu Trp Phe Asp Ser Glu Arg Val Lys Ala Pro Leu Ala Arg Leu Cys		
	195	200 205
Ser Glu Ile Gly Ala Pro Pro Ser Gln Lys Gly Ser Ser Ser Gly Met		
	210	215 220
Met Met Val Ala Met Arg His Leu Glu Gly Ile Ala Arg Pro Lys Gly		
225	230	235 240
Gly Thr Gly Ala Leu Thr Glu Ala Leu Val Lys Leu Val Gln Ala Gln		
	245	250 255
Gly Gly Lys Ile Leu Thr Asp Gln Thr Val Lys Arg Val Leu Val Glu		

260	265	270
Asn Asn Gln Ala Ile Gly Val Glu Val Ala Asn Gly Glu Gln Tyr Arg		
275	280	285
Ala Lys Lys Gly Val Ile Ser Asn Ile Asp Ala Arg Arg Leu Phe Leu		
290	295	300
Gln Leu Val Glu Pro Gly Ala Leu Ala Lys Val Asn Gln Asn Leu Gly		
305	310	315
Glu Arg Leu Glu Arg Arg Thr Val Asn Asn Asn Glu Ala Ile Leu Lys		
325	330	335
Ile Asp Cys Ala Leu Ser Gly Leu Pro His Phe Thr Ala Met Ala Gly		
340	345	350
Pro Glu Asp Leu Thr Gly Thr Ile Leu Ile Ala Asp Ser Val Arg His		
355	360	365
Val Glu Glu Ala His Ala Leu Ile Ala Leu Gly Gln Ile Pro Asp Ala		
370	375	380
Asn Pro Ser Leu Tyr Leu Asp Ile Pro Thr Val Leu Asp Pro Thr Met		
385	390	395
Ala Pro Pro Gly Gln His Thr Leu Trp Ile Glu Phe Phe Ala Pro Tyr		
405	410	415
Arg Ile Ala Gly Leu Glu Gly Thr Gly Leu Met Gly Thr Gly Trp Thr		
420	425	430
Asp Glu Leu Lys Glu Lys Val Ala Asp Arg Val Ile Asp Lys Leu Thr		
435	440	445
Asp Tyr Ala Pro Asn Leu Lys Ser Leu Ile Ile Gly Arg Arg Val Glu		
450	455	460
Ser Pro Ala Glu Leu Ala Gln Arg Leu Gly Ser Tyr Asn Gly Asn Val		
465	470	475
Tyr His Leu Asp Met Ser Leu Asp Gln Met Met Phe Leu Arg Pro Leu		
485	490	495

Pro Glu Ile Ala Asn Tyr Gln Thr Pro Ile Lys Asn Leu Tyr Leu Thr
 500 505 510

Gly Ala Gly Thr His Pro Gly Gly Ser Ile Ser Gly Met Pro Gly Arg
 515 520 525

Asn Cys Ala Arg Val Phe Leu Lys Gln Gln Arg Arg Phe Trp
 530 535 540

<210> 23
 <211> 776
 <212> DNA
 <213> Bradyrhizobium sp.

<220>
 <221> CDS
 <222> (1)..(774)

<400> 23
 atg cat gca gca acc gcc aag gct act gag ttc ggg gcc tct cgg cgc 48
 Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg
 1 5 10 15
 gac gat gcg agg cag cgc cgc gtc ggt ctc acg ctg gcc gcg gtc atc 96
 Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile
 20 25 30
 atc gcc gcc tgg ctg gtg ctg cat gtc ggt ctg atg ttc ttc tgg ccg 144
 Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
 35 40 45
 ctg acc ctt cac agc ctg ctg ccg gct ttg cct ctg gtg gtg ctg cag 192
 Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln
 50 55 60
 acc tgg ctc tat gta ggc ctg ttc atc atc gcg cat gac tgc atg cac 240
 Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
 65 70 75 80
 ggc tcg ctg gtg ccg ttc aag ccg cag gtc aac cgc cgt atc gga cag 288
 Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
 85 90 95
 ctc tgc ctg ttc ctc tat gcc ggg ttc tcc ttc gac gct ctc aat gtc 336
 Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
 100 105 110
 gag cac cac aag cat cac cgc cat ccc gcc acg gcc gag gat ccc gat 384
 Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp
 115 120 125

ttc gac gag gtg ccg ccg cac ggc ttc tgg cac tgg ttc gcc agc ttt 432
 Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe
 130 135 140

ttc ctg cac tat ttc ggc tgg aag cag gtc gcg atc atc gca gcc gtc 480
 Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val
 145 150 155 160

tcg ctg gtt tat cag ctc gtc ttc gcc gtt ccc ttg cag aac atc ctg 528
 Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu
 165 170 175

ctg ttc tgg gcg ctg ccc ggg ctg ctg tcg gcg ctg cag ctg ttc acc 576
 Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
 180 185 190

ttc ggc acc tat ctg ccg cac aag ccg gcc acg cag ccc ttc gcc gat 624
 Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
 195 200 205

cgc cac aac gcg cgg acg agc gaa ttt ccc gcg tgg ctg tcg ctg ctg 672
 Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
 210 215 220

acc tgc ttc cac ttc ggc ttt cat cac gag cat cat ctg cat ccc gat 720
 Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
 225 230 235 240

gcg ccg tgg tgg cgg ctg ccg gag atc aag cgg cgg gcc ctg gaa agg 768
 Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
 245 250 255

cgt gac ta 776
 Arg Asp

<210> 24
 <211> 258
 <212> PRT
 <213> Bradyrhizobium sp.

<400> 24

Met His Ala Ala Thr Ala Lys Ala Thr Glu Phe Gly Ala Ser Arg Arg
 1 5 10 15

Asp Asp Ala Arg Gln Arg Arg Val Gly Leu Thr Leu Ala Ala Val Ile
 20 25 30

Ile Ala Ala Trp Leu Val Leu His Val Gly Leu Met Phe Phe Trp Pro
 35 40 45

Leu Thr Leu His Ser Leu Leu Pro Ala Leu Pro Leu Val Val Leu Gln

50

55

60

Thr Trp Leu Tyr Val Gly Leu Phe Ile Ile Ala His Asp Cys Met His
65 70 75 80

Gly Ser Leu Val Pro Phe Lys Pro Gln Val Asn Arg Arg Ile Gly Gln
85 90 95

Leu Cys Leu Phe Leu Tyr Ala Gly Phe Ser Phe Asp Ala Leu Asn Val
100 105 110

Glu His His Lys His His Arg His Pro Gly Thr Ala Glu Asp Pro Asp
115 120 125

Phe Asp Glu Val Pro Pro His Gly Phe Trp His Trp Phe Ala Ser Phe
130 135 140

Phe Leu His Tyr Phe Gly Trp Lys Gln Val Ala Ile Ile Ala Ala Val
145 150 155 160

Ser Leu Val Tyr Gln Leu Val Phe Ala Val Pro Leu Gln Asn Ile Leu
165 170 175

Leu Phe Trp Ala Leu Pro Gly Leu Leu Ser Ala Leu Gln Leu Phe Thr
180 185 190

Phe Gly Thr Tyr Leu Pro His Lys Pro Ala Thr Gln Pro Phe Ala Asp
195 200 205

Arg His Asn Ala Arg Thr Ser Glu Phe Pro Ala Trp Leu Ser Leu Leu
210 215 220

Thr Cys Phe His Phe Gly Phe His His Glu His His Leu His Pro Asp
225 230 235 240

Ala Pro Trp Trp Arg Leu Pro Glu Ile Lys Arg Arg Ala Leu Glu Arg
245 250 255

Arg Asp

<210> 25

<211> 777

<212> DNA
 <213> Nostoc sp.

<220>
 <221> CDS
 <222> (1) .. (777)

<400> 25
 atg gtt cag tgt caa cca tca tct ctg cat tca gaa aaa ctg gtg tta 48
 Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu
 1 5 10 15

ttg tca tgc aca atc aga gat gat aaa aat att aat aag ggt ata ttt 96
 Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe
 20 25 30

att gcc tgc ttt atc tta ttt tta tgg gca att agt tta atc tta tta 144
 Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
 35 40 45

ctc tca ata gat aca tcc ata att cat aag agc tta tta ggt ata gcc 192
 Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala
 50 55 60

atg ctt tgg cag acc ttc tta tat aca ggt tta ttt att act gct cat 240
 Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80

gat gcc atg cac ggc gta gtt tat ccc aaa aat ccc aga ata aat aat 288
 Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
 85 90 95

ttt ata ggt aag ctc act cta atc ttg tat gga cta ctc cct tat aaa 336
 Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
 100 105 110

gat tta ttg aaa aaa cat tgg tta cac cac gga cat cct ggt act gat 384
 Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp
 115 120 125

tta gac cct gat tat tac aat ggt cat ccc caa aac ttc ttt ctt tgg 432
 Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp
 130 135 140

tat cta cat ttt atg aag tct tat tgg cga tgg acg caa att ttc gga 480
 Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly
 145 150 155 160

tta gtg atg att ttt cat gga ctt aaa aat ctg gtg cat ata cca gaa 528
 Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu
 165 170 175

aat aat tta att ata ttt tgg atg ata cct tct att tta agt tca gta 576
 Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val
 180 185 190

caa cta ttt tat ttt ggt aca ttt ttg cct cat aaa aag cta gaa ggt 624
 Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly
 195 200 205

ggt tat act aac ccc cat tgt gcg cgc agt atc cca tta cct ctt ttt 672
 Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe
 210 215 220

tgg tct ttt gtt act tgt tat cac ttc ggc tac cac aag gaa cat cac 720
 Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His
 225 230 235 240

gaa tac cct caa ctt cct tgg tgg aaa tta cct gaa gct cac aaa ata 768
 Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile
 245 250 255

tct tta taa 777
 Ser Leu

<210> 26
 <211> 258
 <212> PRT
 <213> Nostoc sp.

<400> 26

Met Val Gln Cys Gln Pro Ser Ser Leu His Ser Glu Lys Leu Val Leu
 1 5 10 15

Leu Ser Ser Thr Ile Arg Asp Asp Lys Asn Ile Asn Lys Gly Ile Phe
 20 25 30

Ile Ala Cys Phe Ile Leu Phe Leu Trp Ala Ile Ser Leu Ile Leu Leu
 35 40 45

Leu Ser Ile Asp Thr Ser Ile Ile His Lys Ser Leu Leu Gly Ile Ala
 50 55 60

Met Leu Trp Gln Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His
 65 70 75 80

Asp Ala Met His Gly Val Val Tyr Pro Lys Asn Pro Arg Ile Asn Asn
 85 90 95

Phe Ile Gly Lys Leu Thr Leu Ile Leu Tyr Gly Leu Leu Pro Tyr Lys
 100 105 110

Asp Leu Leu Lys Lys His Trp Leu His His Gly His Pro Gly Thr Asp

115	120	125
Leu Asp Pro Asp Tyr Tyr Asn Gly His Pro Gln Asn Phe Phe Leu Trp		
130	135	140
Tyr Leu His Phe Met Lys Ser Tyr Trp Arg Trp Thr Gln Ile Phe Gly		
145	150	155 160
Leu Val Met Ile Phe His Gly Leu Lys Asn Leu Val His Ile Pro Glu		
	165	170 175
Asn Asn Leu Ile Ile Phe Trp Met Ile Pro Ser Ile Leu Ser Ser Val		
	180	185 190
Gln Leu Phe Tyr Phe Gly Thr Phe Leu Pro His Lys Lys Leu Glu Gly		
	195	200 205
Gly Tyr Thr Asn Pro His Cys Ala Arg Ser Ile Pro Leu Pro Leu Phe		
	210	215 220
Trp Ser Phe Val Thr Cys Tyr His Phe Gly Tyr His Lys Glu His His		
	225	230 235 240
Glu Tyr Pro Gln Leu Pro Trp Trp Lys Leu Pro Glu Ala His Lys Ile		
	245	250 255
Ser Leu		

<210> 27
 <211> 789
 <212> DNA
 <213> Nostoc punctiforme

<220>
 <221> CDS
 <222> (1) .. (789)

<400> 27	
ttg aat ttt tgt gat aaa cca gtt agc tat tat gtt gca ata gag caa	48
Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln	
1 5 10 15	
tta agt gct aaa gaa gat act gtt tgg ggg ctg gtg att gtc ata gta	96
Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val	

20	25	30	
att att agt ctt tgg gta gct agt ttg gct ttt tta cta gct att aat Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn 35 40 45			144
tat gcc aaa gtc cca att tgg ttg ata cct att gca ata gtt tgg caa Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln 50 55 60			192
atg ttc ctt tat aca ggg cta ttt att act gca cat gat gct atg cat Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His 65 70 75 80			240
ggg tca gtt tat cgt aaa aat ccc aaa att aat aat ttt atc ggt tca Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser 85 90 95			288
cta gct gta gcg ctt tac gct gtg ttt cca tat caa cag atg tta aag Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys 100 105 110			336
aat cat tgc tta cat cat cgt cat cct gct agc gaa gtt gac cca gat Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp 115 120 125			384
ttt cat gat ggt aag aga aca aac gct att ttc tgg tat ctc cat ttc Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe 130 135 140			432
atg ata gaa tac tcc agt tgg caa cag tta ata gta cta act atc cta Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu 145 150 155 160			480
ttt aat tta gct aaa tac gtt ttg cac atc cat caa ata aat ctc atc Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile 165 170 175			528
tta ttt tgg agt att cct cca att tta agt tcc att caa ctg ttt tat Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr 180 185 190			576
ttc gga aca ttt ttg cct cat cga gaa ccc aag aaa gga tat gtt tat Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr 195 200 205			624
ccc cat tgc agc caa aca ata aaa ttg cca act ttt ttg tca ttt atc Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile 210 215 220			672
gct tgc tac cac ttt ggt tat cat gaa gaa cat cat gag tat ccc cat Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His 225 230 235 240			720
gta cct tgg tgg caa ctt cca tct gta tat aag cag aga gta ttc aac Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn 245 250 255			768

aat tca gta acc aat tcg taa
 Asn Ser Val Thr Asn Ser
 260

789

<210> 28
 <211> 262
 <212> PRT
 <213> Nostoc punctiforme

<400> 28

Leu Asn Phe Cys Asp Lys Pro Val Ser Tyr Tyr Val Ala Ile Glu Gln
 1 5 10 15

Leu Ser Ala Lys Glu Asp Thr Val Trp Gly Leu Val Ile Val Ile Val
 20 25 30

Ile Ile Ser Leu Trp Val Ala Ser Leu Ala Phe Leu Leu Ala Ile Asn
 35 40 45

Tyr Ala Lys Val Pro Ile Trp Leu Ile Pro Ile Ala Ile Val Trp Gln
 50 55 60

Met Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ala His Asp Ala Met His
 65 70 75 80

Gly Ser Val Tyr Arg Lys Asn Pro Lys Ile Asn Asn Phe Ile Gly Ser
 85 90 95

Leu Ala Val Ala Leu Tyr Ala Val Phe Pro Tyr Gln Gln Met Leu Lys
 100 105 110

Asn His Cys Leu His His Arg His Pro Ala Ser Glu Val Asp Pro Asp
 115 120 125

Phe His Asp Gly Lys Arg Thr Asn Ala Ile Phe Trp Tyr Leu His Phe
 130 135 140

Met Ile Glu Tyr Ser Ser Trp Gln Gln Leu Ile Val Leu Thr Ile Leu
 145 150 155 160

Phe Asn Leu Ala Lys Tyr Val Leu His Ile His Gln Ile Asn Leu Ile
 165 170 175

Leu Phe Trp Ser Ile Pro Pro Ile Leu Ser Ser Ile Gln Leu Phe Tyr
 180 185 190

Phe Gly Thr Phe Leu Pro His Arg Glu Pro Lys Lys Gly Tyr Val Tyr
 195 200 205

Pro His Cys Ser Gln Thr Ile Lys Leu Pro Thr Phe Leu Ser Phe Ile
 210 215 220

Ala Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His
 225 230 235 240

Val Pro Trp Trp Gln Leu Pro Ser Val Tyr Lys Gln Arg Val Phe Asn
 245 250 255

Asn Ser Val Thr Asn Ser
 260

<210> 29
 <211> 762
 <212> DNA
 <213> Nostoc punctiforme

<220>
 <221> CDS
 <222> (1) .. (762)

<400> 29
 gtg atc cag tta gaa caa cca ctc agt cat caa gca aaa ctg act cca 48
 Val Ile Gln Leu Glu Gln Pro Leu Ser His Gln Ala Lys Leu Thr Pro
 1 5 10 15
 gta ctg aga agt aaa tct cag ttt aag ggg ctt ttc att gct att gtc 96
 Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val
 20 25 30
 att gtt agc gca tgg gtc att agc ctg agt tta tta ctt tcc ctt gac 144
 Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp
 35 40 45
 atc tca aag cta aaa ttt tgg atg tta ttg cct gtt ata cta tgg caa 192
 Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln
 50 55 60
 aca ttt tta tat acg gga tta ttt att aca tct cat gat gcc atg cat 240
 Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His
 65 70 75 80
 ggc gta gta ttt ccc caa aac acc aag att aat cat ttg att gga aca 288
 Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr

85										90					95					
ttg acc cta tcc ctt tat ggt ctt tta cca tat caa aaa cta ttg aaa	336																			
Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys																				
100	105	110																		
aaa cat tgg tta cac cac cac aat cca gca agc tca ata gac ccg gat	384																			
Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp																				
115	120	125																		
ttt cac aat ggt aaa cac caa agt ttc ttt gct tgg tat ttt cat ttt	432																			
Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe																				
130	135	140																		
atg aaa ggt tac tgg agt tgg ggg caa ata att gcg ttg act att att	480																			
Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile																				
145	150	155	160																	
tat aac ttt gct aaa tac ata ctc cat atc cca agt gat aat cta act	528																			
Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr																				
165	170	175																		
tac ttt tgg gtg cta ccc tcg ctt tta agt tca tta caa tta ttc tat	576																			
Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr																				
180	185	190																		
ttt ggt act ttt tta ccc cat agt gaa cca ata ggg ggt tat gtt cag	624																			
Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln																				
195	200	205																		
cct cat tgt gcc caa aca att agc cgt cct att tgg tgg tca ttt atc	672																			
Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile																				
210	215	220																		
acg tgc tat cat ttt ggc tac cac gag gaa cat cac gaa tat cct cat	720																			
Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His																				
225	230	235	240																	
att tct tgg tgg cag tta cca gaa att tac aaa gca aaa tag	762																			
Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys																				
245	250																			

<210> 30

<211> 253

<212> PRT

<213> Nostoc punctiforme

<400> 30

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1 5 10 15

Val Leu Arg Ser Lys Ser Gln Phe Lys Gly Leu Phe Ile Ala Ile Val

20	25	30
Ile Val Ser Ala Trp Val Ile Ser Leu Ser Leu Leu Leu Ser Leu Asp 35 40 45		
Ile Ser Lys Leu Lys Phe Trp Met Leu Leu Pro Val Ile Leu Trp Gln 50 55 60		
Thr Phe Leu Tyr Thr Gly Leu Phe Ile Thr Ser His Asp Ala Met His 65 70 75 80		
Gly Val Val Phe Pro Gln Asn Thr Lys Ile Asn His Leu Ile Gly Thr 85 90 95		
Leu Thr Leu Ser Leu Tyr Gly Leu Leu Pro Tyr Gln Lys Leu Leu Lys 100 105 110		
Lys His Trp Leu His His His Asn Pro Ala Ser Ser Ile Asp Pro Asp 115 120 125		
Phe His Asn Gly Lys His Gln Ser Phe Phe Ala Trp Tyr Phe His Phe 130 135 140		
Met Lys Gly Tyr Trp Ser Trp Gly Gln Ile Ile Ala Leu Thr Ile Ile 145 150 155 160		
Tyr Asn Phe Ala Lys Tyr Ile Leu His Ile Pro Ser Asp Asn Leu Thr 165 170 175		
Tyr Phe Trp Val Leu Pro Ser Leu Leu Ser Ser Leu Gln Leu Phe Tyr 180 185 190		
Phe Gly Thr Phe Leu Pro His Ser Glu Pro Ile Gly Gly Tyr Val Gln 195 200 205		
Pro His Cys Ala Gln Thr Ile Ser Arg Pro Ile Trp Trp Ser Phe Ile 210 215 220		
Thr Cys Tyr His Phe Gly Tyr His Glu Glu His His Glu Tyr Pro His 225 230 235 240		
Ile Ser Trp Trp Gln Leu Pro Glu Ile Tyr Lys Ala Lys 245 250		

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 <212> DNA
 <213> Haematococcus pluvialis

<220>
 <221> CDS
 <222> (3)..(971)

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 Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile
 1 5 10 15

ggc cca cct cct cat ctc cat cgg tca ttt gct gct acc acg atg ctg 95
 Gly Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu
 20 25 30

tcg aag ctg cag tca atc agc gtc aag gcc cgc cgc gtt gaa cta gcc 143
 Ser Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala
 35 40 45

cgc gac atc acg cgg ccc aaa gtc tgc ctg cat gct cag cgg tgc tcg 191
 Arg Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser
 50 55 60

tta gtt cgg ctg cga gtg gca gca cca cag aca gag gag gcg ctg gga 239
 Leu Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly
 65 70 75

acc gtg cag gct gcc ggc gcg ggc gat gag cac agc gcc gat gta gca 287
 Thr Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala
 80 85 90 95

ctc cag cag ctt gac cgg gct atc gca gag cgt cgt gcc cgg cgc aaa 335
 Leu Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys
 100 105 110

cgg gag cag ctg tca tac cag gct gcc gcc att gca gca tca att ggc 383
 Arg Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly
 115 120 125

gtg tca ggc att gcc atc ttc gcc acc tac ctg aga ttt gcc atg cac 431
 Val Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His
 130 135 140

atg acc gtg ggc ggc gca gtg cca tgg ggt gaa gtg gct ggc act ctc 479
 Met Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu
 145 150 155

ctc ttg gtg gtt ggt ggc gcg ctc ggc atg gag atg tat gcc cgc tat 527
 Leu Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr
 160 165 170 175

gca cac aaa gcc atc tgg cat gag tcg cct ctg ggc tgg ctg ctg cac Ala His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His 180 185 190	575
aag agc cac cac aca cct cgc act gga ccc ttt gaa gcc aac gac ttg Lys Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu 195 200 205	623
ttt gca atc atc aat gga ctg ccc gcc atg ctc ctg tgt acc ttt ggc Phe Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly 210 215 220	671
ttc tgg ctg ccc aac gtc ctg ggg gcg gcc tgc ttt gga gcg ggg ctg Phe Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu 225 230 235	719
ggc atc acg cta tac ggc atg gca tat atg ttt gta cac gat ggc ctg Gly Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu 240 245 250 255	767
gtg cac agg cgc ttt ccc acc ggg ccc atc gct ggc ctg ccc tac atg Val His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met 260 265 270	815
aag cgc ctg aca gtg gcc cac cag cta cac cac agc ggc aag tac ggt Lys Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly 275 280 285	863
ggc gcg ccc tgg ggt atg ttc ttg ggt cca cag gag ctg cag cac att Gly Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile 290 295 300	911
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tcc aag cgg tag ggtgcggaac caggcacgct ggtttcacac ctcatgcctg Ser Lys Arg 320	1011
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<210> 32
 <211> 322
 <212> PRT
 <213> Haematococcus pluvialis

<400> 32

Thr Phe His Lys Pro Val Ser Gly Ala Ser Ala Leu Pro His Ile Gly
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Pro Pro Pro His Leu His Arg Ser Phe Ala Ala Thr Thr Met Leu Ser
 20 25 30

Lys Leu Gln Ser Ile Ser Val Lys Ala Arg Arg Val Glu Leu Ala Arg
 35 40 45

Asp Ile Thr Arg Pro Lys Val Cys Leu His Ala Gln Arg Cys Ser Leu
 50 55 60

Val Arg Leu Arg Val Ala Ala Pro Gln Thr Glu Glu Ala Leu Gly Thr
 65 70 75 80

Val Gln Ala Ala Gly Ala Gly Asp Glu His Ser Ala Asp Val Ala Leu
 85 90 95

Gln Gln Leu Asp Arg Ala Ile Ala Glu Arg Arg Ala Arg Arg Lys Arg
 100 105 110

Glu Gln Leu Ser Tyr Gln Ala Ala Ala Ile Ala Ala Ser Ile Gly Val
 115 120 125

Ser Gly Ile Ala Ile Phe Ala Thr Tyr Leu Arg Phe Ala Met His Met
 130 135 140

Thr Val Gly Gly Ala Val Pro Trp Gly Glu Val Ala Gly Thr Leu Leu
 145 150 155 160

Leu Val Val Gly Gly Ala Leu Gly Met Glu Met Tyr Ala Arg Tyr Ala
 165 170 175

His Lys Ala Ile Trp His Glu Ser Pro Leu Gly Trp Leu Leu His Lys
 180 185 190

Ser His His Thr Pro Arg Thr Gly Pro Phe Glu Ala Asn Asp Leu Phe
 195 200 205

Ala Ile Ile Asn Gly Leu Pro Ala Met Leu Leu Cys Thr Phe Gly Phe
 210 215 220

Trp Leu Pro Asn Val Leu Gly Ala Ala Cys Phe Gly Ala Gly Leu Gly
 225 230 235 240

Ile Thr Leu Tyr Gly Met Ala Tyr Met Phe Val His Asp Gly Leu Val
 245 250 255

His Arg Arg Phe Pro Thr Gly Pro Ile Ala Gly Leu Pro Tyr Met Lys
 260 265 270

Arg Leu Thr Val Ala His Gln Leu His His Ser Gly Lys Tyr Gly Gly
 275 280 285

Ala Pro Trp Gly Met Phe Leu Gly Pro Gln Glu Leu Gln His Ile Pro
 290 295 300

Gly Ala Ala Glu Glu Val Glu Arg Leu Val Leu Glu Leu Asp Trp Ser
 305 310 315 320

Lys Arg

<210> 33
 <211> 528
 <212> DNA
 <213> Erwinia uredovora

<220>
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 atg gaa gtg att gct gca ctg gca cac aaa tac atc atg cac ggc tgg 96
 Met Glu Val Ile Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
 20 25 30

ggt tgg gga tgg cat ctt tca cat cat gaa ccg cgt aaa ggt gcg ttt 144
 Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
 35 40 45

gaa gtt aac gat ctt tat gcc gtg gtt ttt gct gca tta tcg atc ctg 192
 Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ala Leu Ser Ile Leu
 50 55 60

ctg att tat ctg ggc agt aca gga atg tgg ccg ctc cag tgg att ggc 240
 Leu Ile Tyr Leu Gly Ser Thr Gly Met Trp Pro Leu Gln Trp Ile Gly
 65 70 75 80

gca ggt atg acg gcg tat gga tta ctc tat ttt atg gtg cac gac ggg 288
 Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
 85 90 95

ctg gtg cat caa cgt tgg cca ttc cgc tat att cca cgc aag ggc tac 336
 Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
 100 105 110

ctc aaa cgg ttg tat atg gcg cac cgt atg cat cac gcc gtc agg ggc 384
 Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
 115 120 125

aaa gaa ggt tgt gtt tct ttt ggc ttc ctc tat gcg ccg ccc ctg tca 432
 Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
 130 135 140

aaa ctt cag gcg acg ctc cgg gaa aga cat ggc gct aga gcg ggc gct 480
 Lys Leu Gln Ala Thr Leu Arg Glu Arg His Gly Ala Arg Ala Gly Ala
 145 150 155 160

gcc aga gat gcg cag ggc ggg gag gat gag ccc gca tcc ggg aag taa 528
 Ala Arg Asp Ala Gln Gly Gly Glu Asp Glu Pro Ala Ser Gly Lys
 165 170 175

<210> 34
 <211> 175
 <212> PRT
 <213> Erwinia uredovora

<400> 34

Met Leu Trp Ile Trp Asn Ala Leu Ile Val Phe Val Thr Val Ile Gly
 1 5 10 15

Met Glu Val Ile Ala Ala Leu Ala His Lys Tyr Ile Met His Gly Trp
 20 25 30

Gly Trp Gly Trp His Leu Ser His His Glu Pro Arg Lys Gly Ala Phe
 35 40 45

Glu Val Asn Asp Leu Tyr Ala Val Val Phe Ala Ala Leu Ser Ile Leu

50

55

60

Leu Ile Tyr Leu Gly Ser Thr Gly Met Trp Pro Leu Gln Trp Ile Gly
65 70 75 80

Ala Gly Met Thr Ala Tyr Gly Leu Leu Tyr Phe Met Val His Asp Gly
85 90 95

Leu Val His Gln Arg Trp Pro Phe Arg Tyr Ile Pro Arg Lys Gly Tyr
100 105 110

Leu Lys Arg Leu Tyr Met Ala His Arg Met His His Ala Val Arg Gly
115 120 125

Lys Glu Gly Cys Val Ser Phe Gly Phe Leu Tyr Ala Pro Pro Leu Ser
130 135 140

Lys Leu Gln Ala Thr Leu Arg Glu Arg His Gly Ala Arg Ala Gly Ala
145 150 155 160

Ala Arg Asp Ala Gln Gly Gly Glu Asp Glu Pro Ala Ser Gly Lys
165 170 175

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<211> 1520
<212> DNA
<213> Artificial Sequence

<220>
<223> Promotor

<400> 35
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tgaattgaag ttgagataaa aaaaaagggg gcccaatttg tcaacgccaa agagtcaagc 180
tttttctttg gctttagccg aacaatctaa gacttattgt ttttgaagat atttgacctt 240
ttctagatat tccttcaagt aaagcttttt tcgagttttt tttttttttc tttgtgaagg 300
atttattggt attggtatcc attttttatt ggaagacaag ataagttaat attgattttg 360
cttaaagatt aaaaggaaat cagaaaacga caataaaaaa tgtaacggac aaactatggt 420
gtcgattata agtctaaatc cttaaaaaat gacaacgagt tgctttcctc tgaaaacaat 480

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tcttttgtct ttgcaagaaa ggtttctttt ttgtttgctt gcattactta aacatcaa 540
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gagtgcaccc taaggaaacta aatgccattc atttgtttta aaacgacatc aaagattgat 660
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gatttaaaaa acaatttctg ctttgaacca aaactttttt tttctcttta atcattaact 1440
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<210> 36
<211> 16245
<212> DNA
<213> Artificial Sequence

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<220>
<223> Plasmid

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<223> n is a, c, g, or t

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<220>

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<221> misc_feature
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 <223> n is a, c, g, or t

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 aaaacttggc cctcactgac agatgagggg cggacgttga cacttgaggg gccgactcac 180
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 caagcctggg gataagtgcc ctgcggtatt gacacttgag gggcgcgact actgacagat 360
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<213> *Blakeslea trispora*

<400> 69

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<211> 882

<212> DNA

<213> Haematococcus pluvialis

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 <211> 528
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 <213> *Erwinia uredovora*

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 gccagagatg cgcagggcgg ggaggatgag cccgcatccg ggaagtaa 528

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 <211> 762
 <212> DNA
 <213> *Nostoc sp. PCC73102*

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 <211> 617
 <212> DNA
 <213> *Haematococcus pluvialis*

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 <213> *Haematococcus pluvialis*

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<210> 77

<211> 2981

<212> DNA

<213> *Blakeslea trispora*

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